622

572 3 522

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alignment_block:
US-09-866-034-2 x HSU31875
                                                                                                                                                                                                               BASE COUNT
ORIGIN
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MEDLINE
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
TITLE
                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
ACCESSION
VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_pr:HSU31875
                                                                                                               Ratio:
Percent Similarity:
                                    Align seg 1/1 to: HSU31875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       794
10 CysAlaArgAlaTrpAsnSerValArgMetAlaSerSerGlyMetThrAr 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAACATCATCAGCTGCAGAGGATTGGGGAGTCAGAGGACTGTGCAGGAAT 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluThrLeuArgIleArgArgLeuGlyGluProGluAspCysAlaGlyIl 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGCGGTGGCAGGC 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eValSerPheLeuCysSerGluAspAlaSerTyrIleThrGlyGluThrV 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTTCAGCAAAGTGTTTCATGGGAATGAGTCTCTCTGGAAGAACTTCAAG
                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 1442)
1 (bases 1 to 1442)
Gabrielli, F., Donadel, G., Bensi, G., Heguy, A. and Melli, M.
A nuclear protein, synthesized in growth-arrested human
A nuclear proteils, is a novel member of the short-chain alcohol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (19-JUL-1995) Franco Gabrielli, Physiology and Biochemistry, University of Pisa, Via Roma 55, Pisa 56126,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Hep27 protein mRNA, complete U31875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dehydrogenase family
Eur. J. Blochem. 232 (2), 473-477 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U31875.1 GI:1079565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gabrielli,F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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3.569
87.833
                                                                                                                                                                                                                                             KTDFSKVFHGNESLMKNPKEHHQLQRIGESEDCAGIVSFLCSPDASYVNGENIAVAGY
STRL*
                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to Streptomyces violaceoruber granaticin polyketide synthase putative ketoacyl, Swiss-Prot Accession Number P16542"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                        codon_start=1
                                                                                                                                                                                                                             369
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                                    from: 1
                                                                                                            Length: 263
Gaps: 2
Percent Identity: 61.597
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cds.
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                                                                                                                                      seq_name: gb_in:AY069779
                                                                           DEFINITION
                                                                                           seg_documentation_block:
LOCUS AY069779
                                                             ACCESSION
                              CEYWORDS
                                                ERSION
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                                                                                                                                                                                           260 AlaSerTyrIleThrGlyGluThrValValValGlyGly 272
                                                                                                                                                                                                                                                                                                                                                           243 lyGluProGluAspCysAlaGlyIleValSerPheLeuCysSerGluAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     523 GAAGGGCGTCCTGGCTAACCGGGTAGCCGTGGTCACGGGGTCCACCAGTG
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                                                                                                                                                                   GCCAGCTACGTCAACGGGAGAACATTGCGGTGGCAGGC
                                                                                                                                                                                                                                 GGGAGTCAGAGGACTGTGCAGGAATCGTGTCCTTCCTGTGCTCTCCAGAT
                                                                                                                                                                                                                                                                                                                            pLysGluLysGluGluSerMetLysGluThrLeuArgIleArgArgLeuG 243
                                                                                                                                                                                                                                                                                                                                                                                                                              ...AGGGGTGCTGTCATCCTGGTCTCTTCCATTGCAGCTTATAATCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTGGGGACCAGTGAGCAGATCTGGGACAAGATCCTAAGTGTGAACGTGA
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                                                            1113 bp mRNA linear
Drosophila melanogașter SD02021 full length cDNA.
AY069779
                             FLI_CDNA
               fruit
                                          AY069779.1 GI:17862893
                                                                                                                                                                                                                                                                                                                                                                                                                          GGCCCCAAGGACATCCGGGTAAACTGC 1069
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922

872 143 822 772

722 93

ORGANISM

Drosophila melanogașter

1219

INV 17-DEC-2001